

Report

	mito.contigs.final
# contigs (>= 0 bp)	2
# contigs (>= 1000 bp)	2
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 0 bp)	181572
Total length (>= 1000 bp)	181572
Total length (>= 5000 bp)	181572
Total length (>= 10000 bp)	181572
Total length (>= 25000 bp)	181572
Total length (>= 50000 bp)	181572
# contigs	2
Largest contig	106645
Total length	181572
Reference length	214261
GC (%)	30.85
Reference GC (%)	30.77
N50	106645
NG50	74927
N75	74927
NG75	74927
L50	1
LG50	2
L75	2
LG75	2
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	84.743
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	0.00
# indels per 100 kbp	0.00
Largest alignment	106645
Total aligned length	181572
NA50	106645
NGA50	74927
NA75	74927
NGA75	74927
LA50	1
LGA50	2
LA75	2
LGA75	2

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

	mito.contigs.final
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	0
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	0
# indels	0
# indels (<= 5 bp)	0
# indels (> 5 bp)	0
Indels length	0

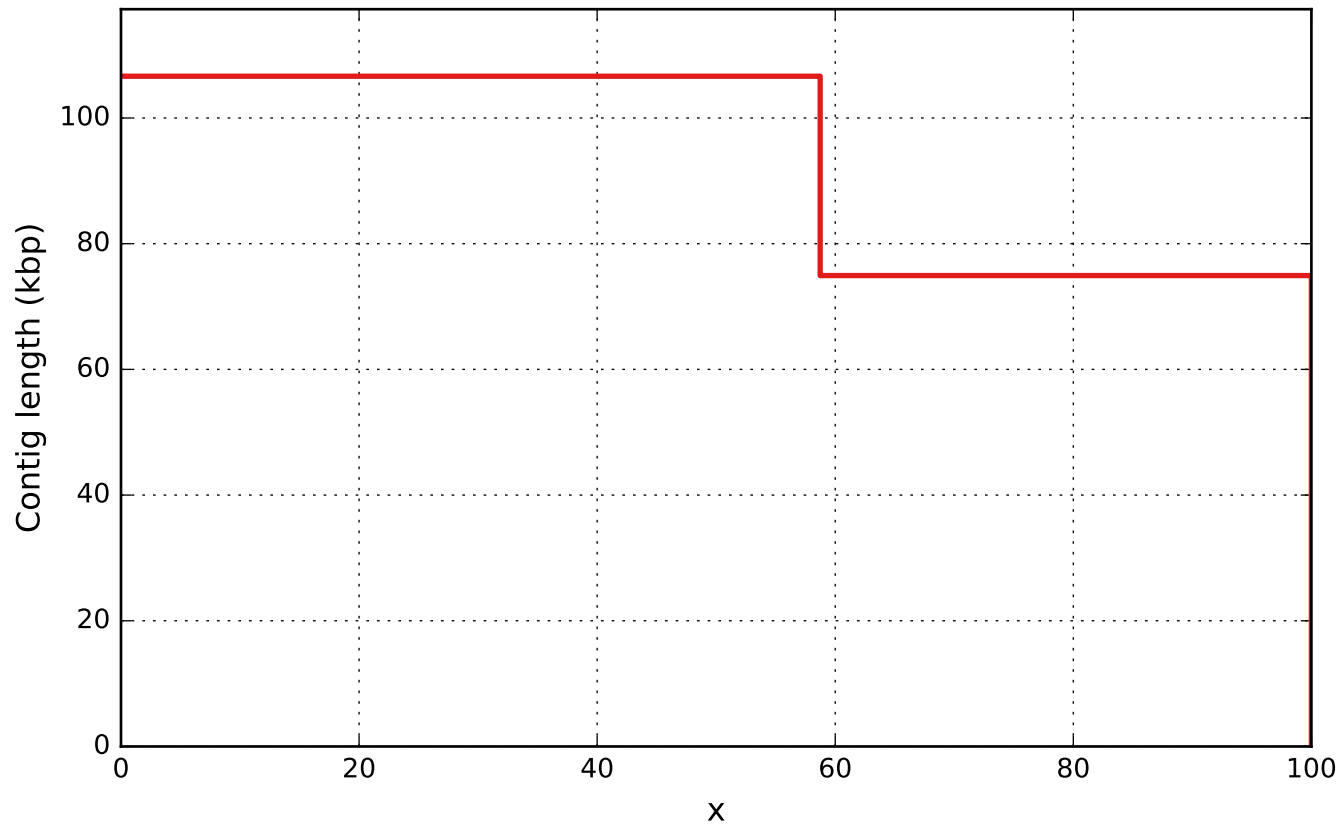
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Unaligned report

	mito.contigs.final
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

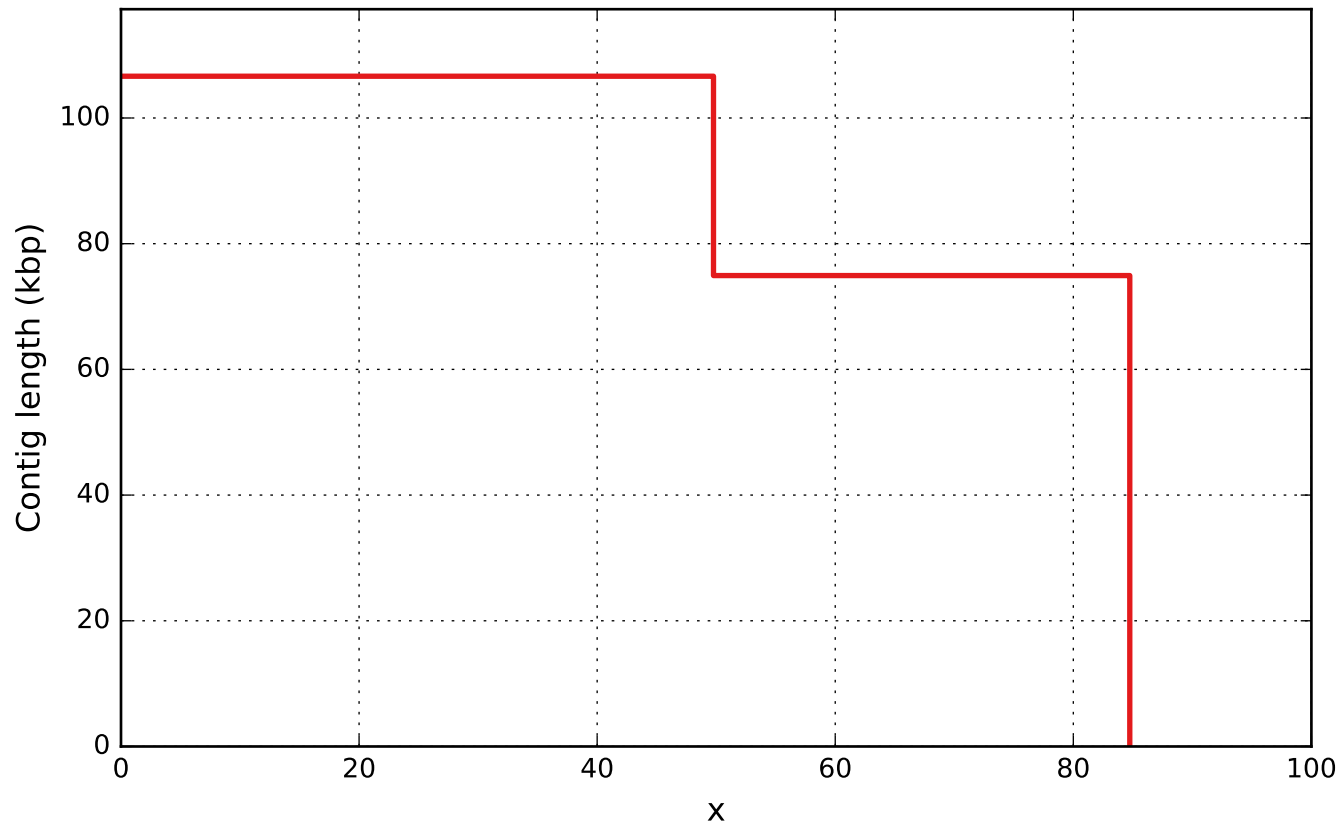
All statistics are based on contigs of size ≥ 500 bp, unless otherwise noted (e.g., "# contigs (≥ 0 bp)" and "Total length (≥ 0 bp)" include all contigs).

Nx



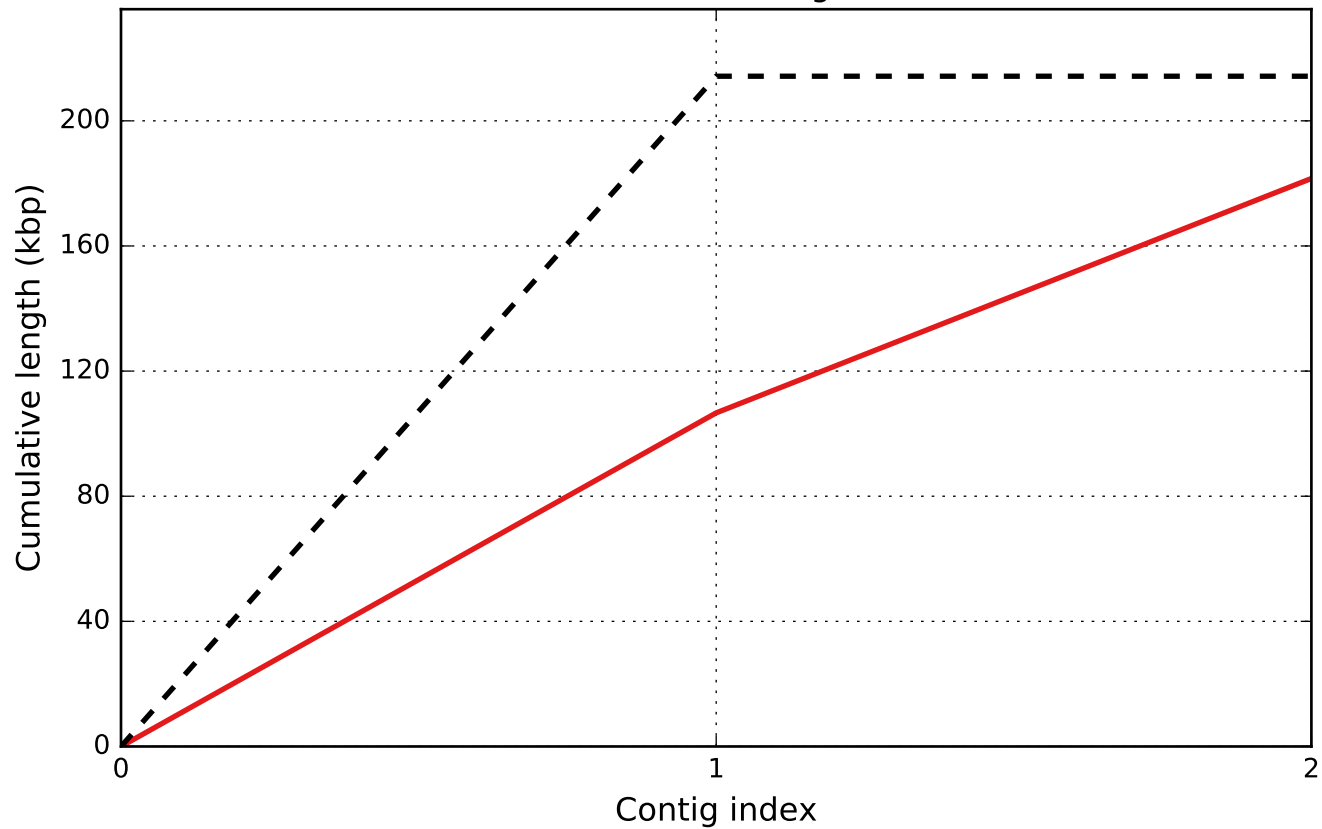
— mito.contigs.final

NGx



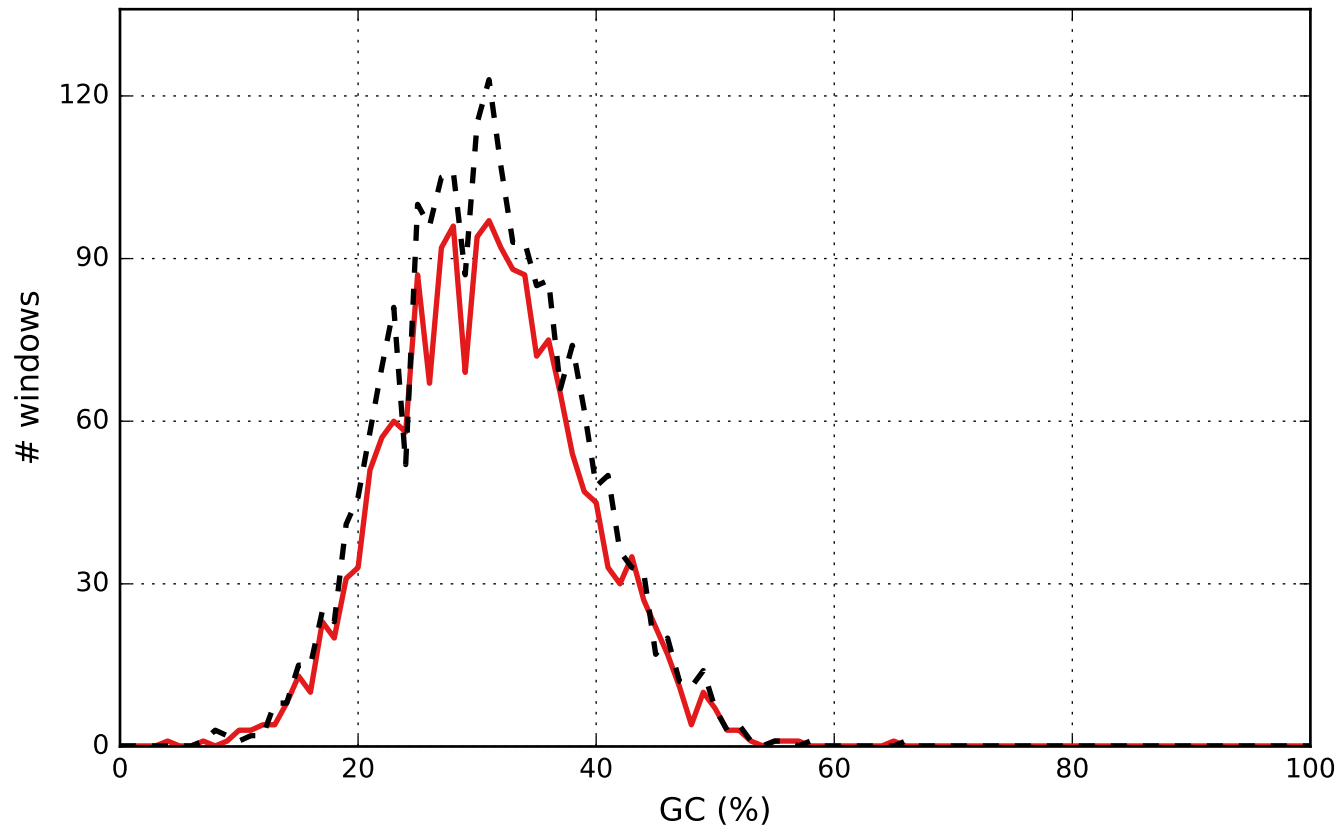
— mito.contigs.final

Cumulative length

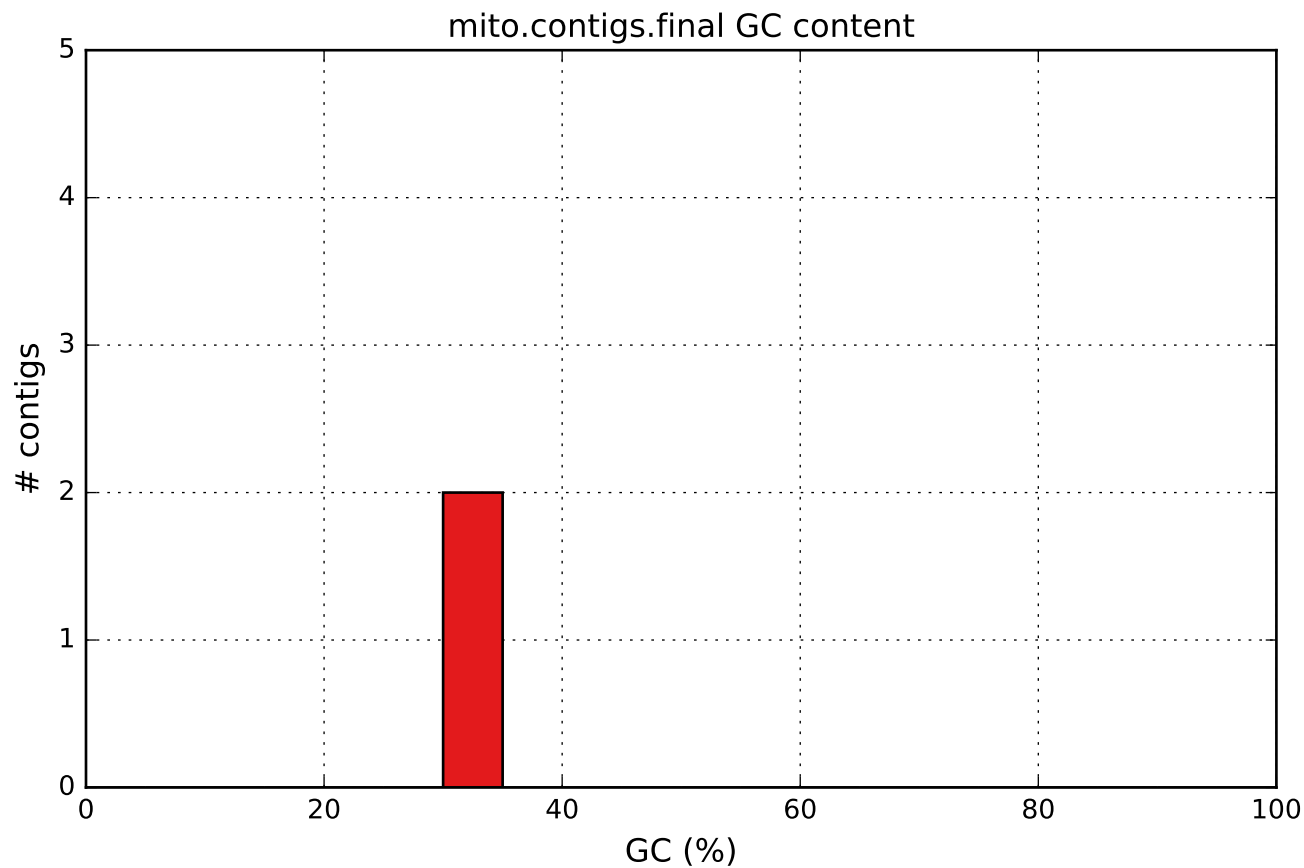


— mito.contigs.final - - Reference

GC content

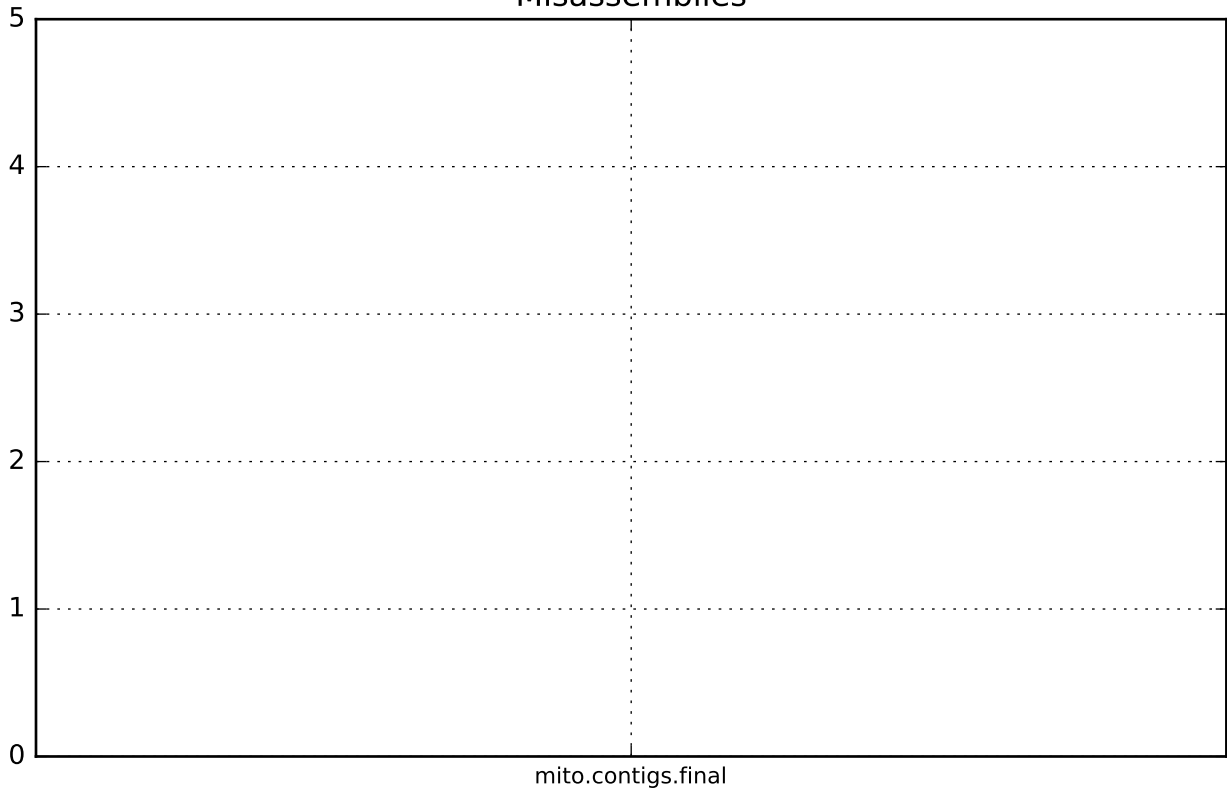


— mito.contigs.final - - Reference

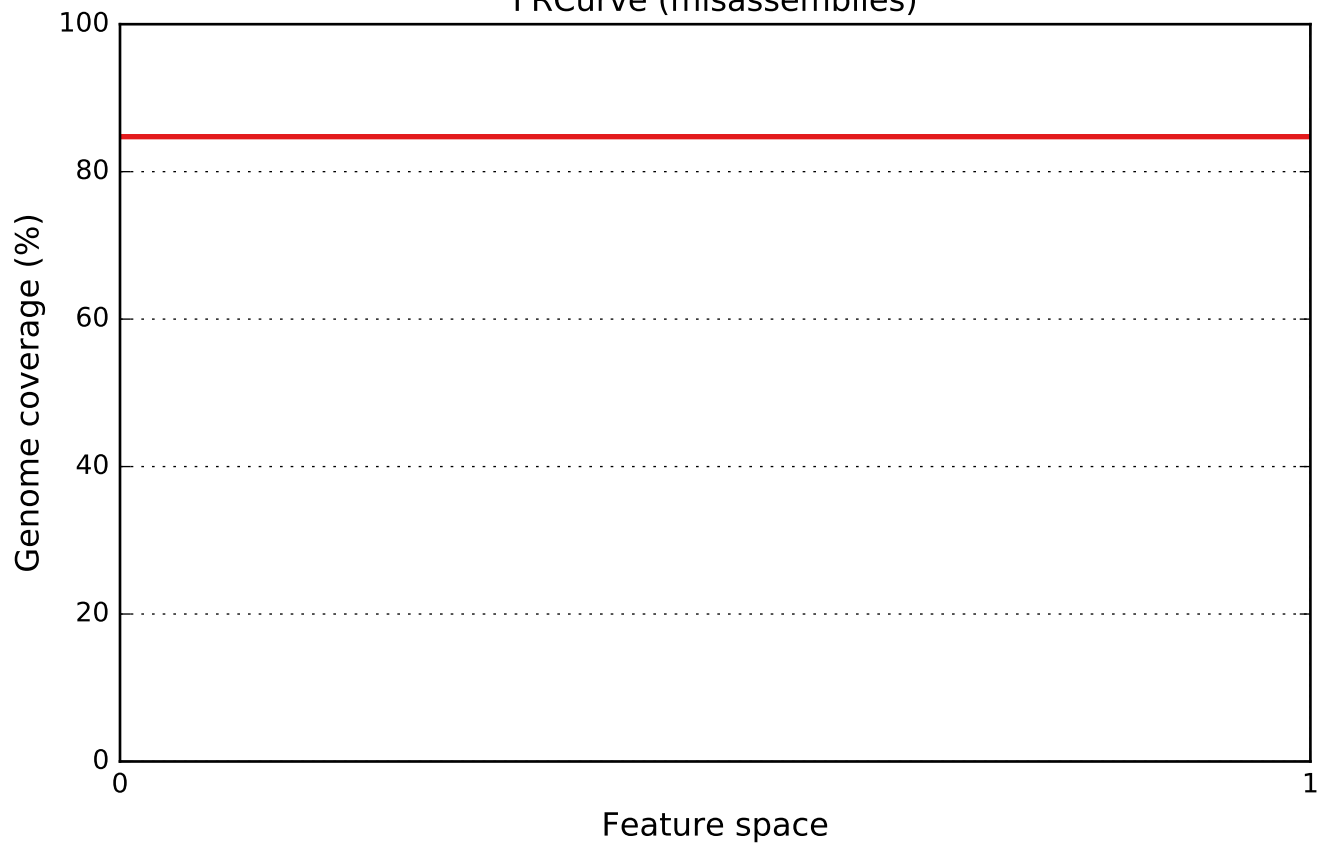


mito.contigs.final

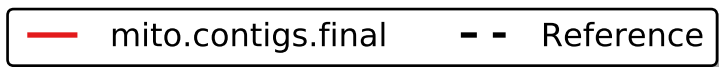
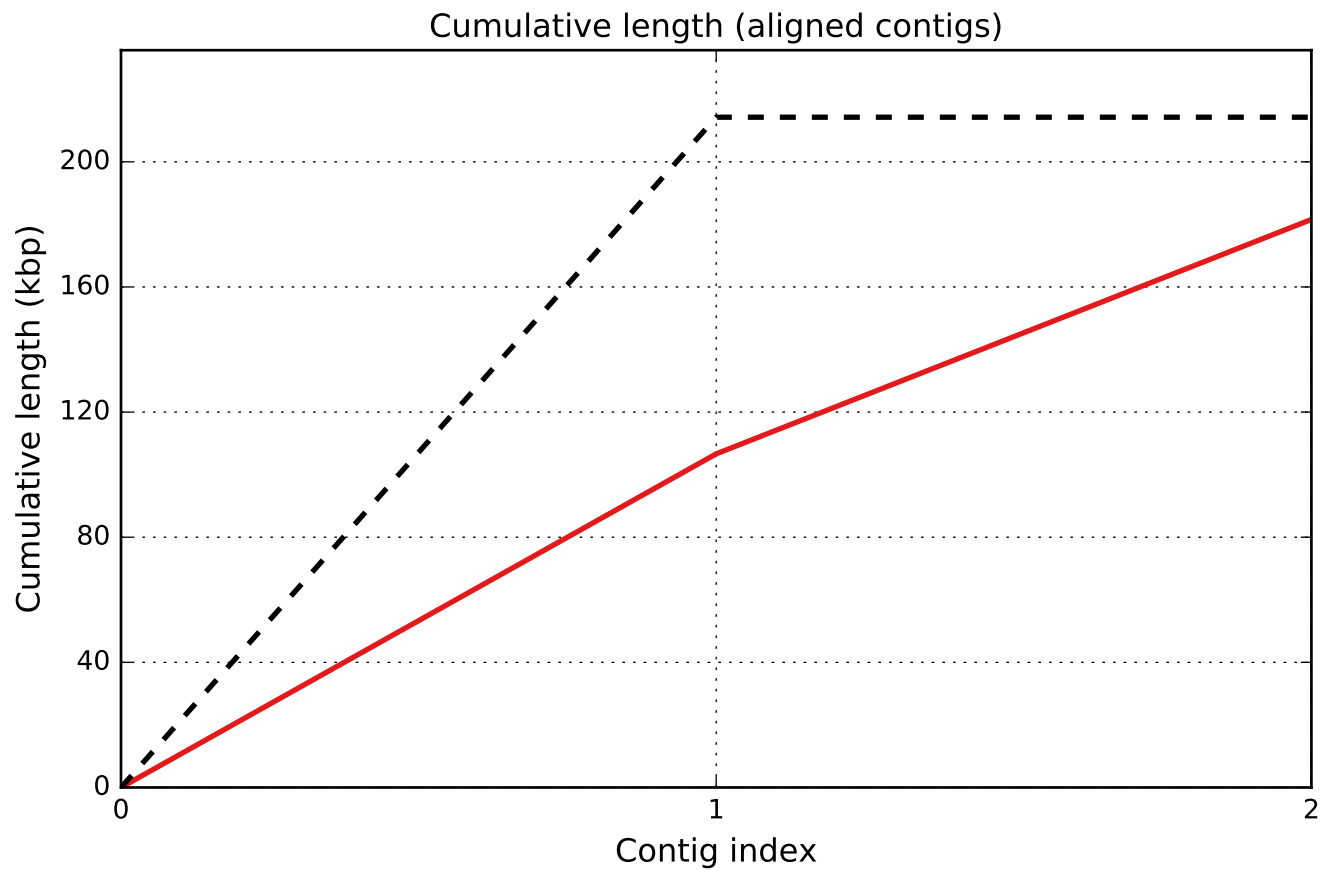
Misassemblies



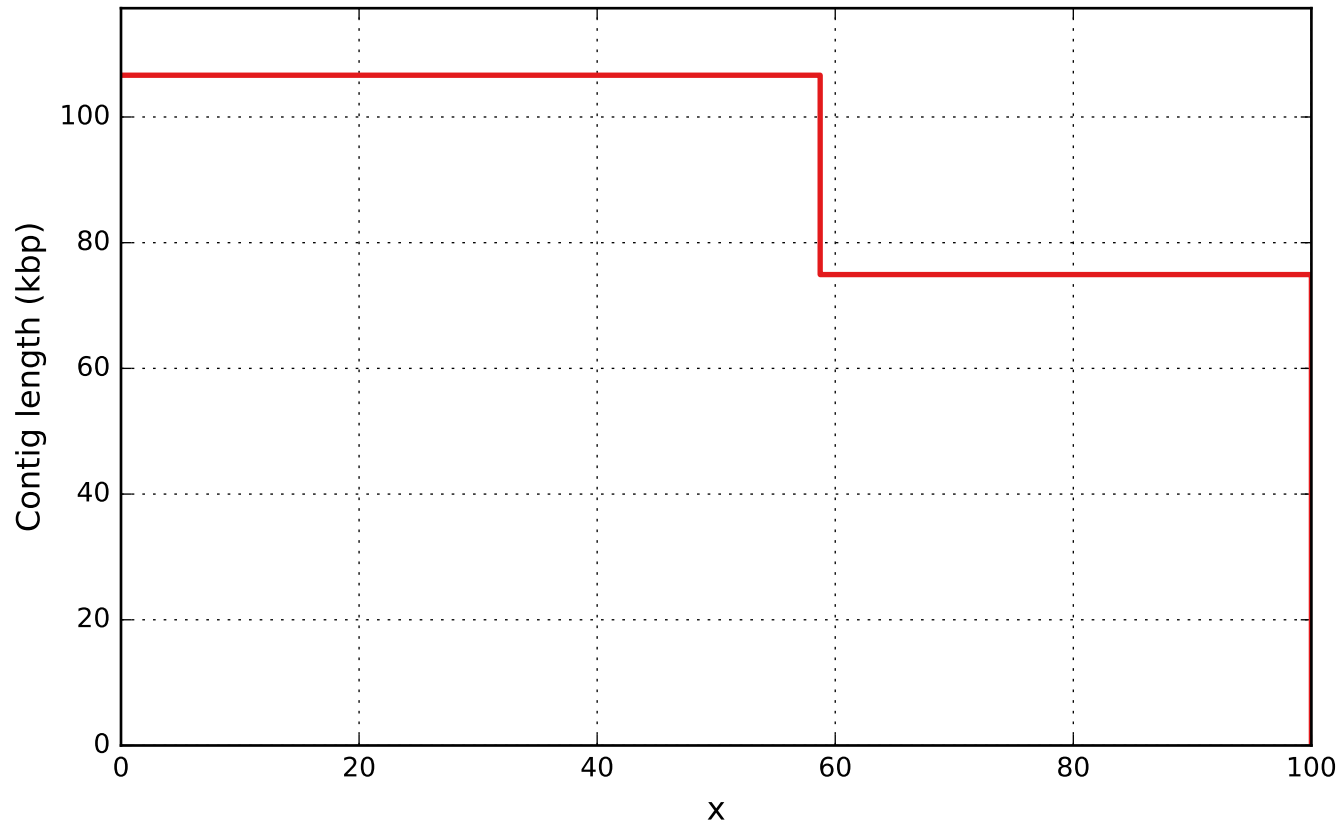
FRCurve (misassemblies)



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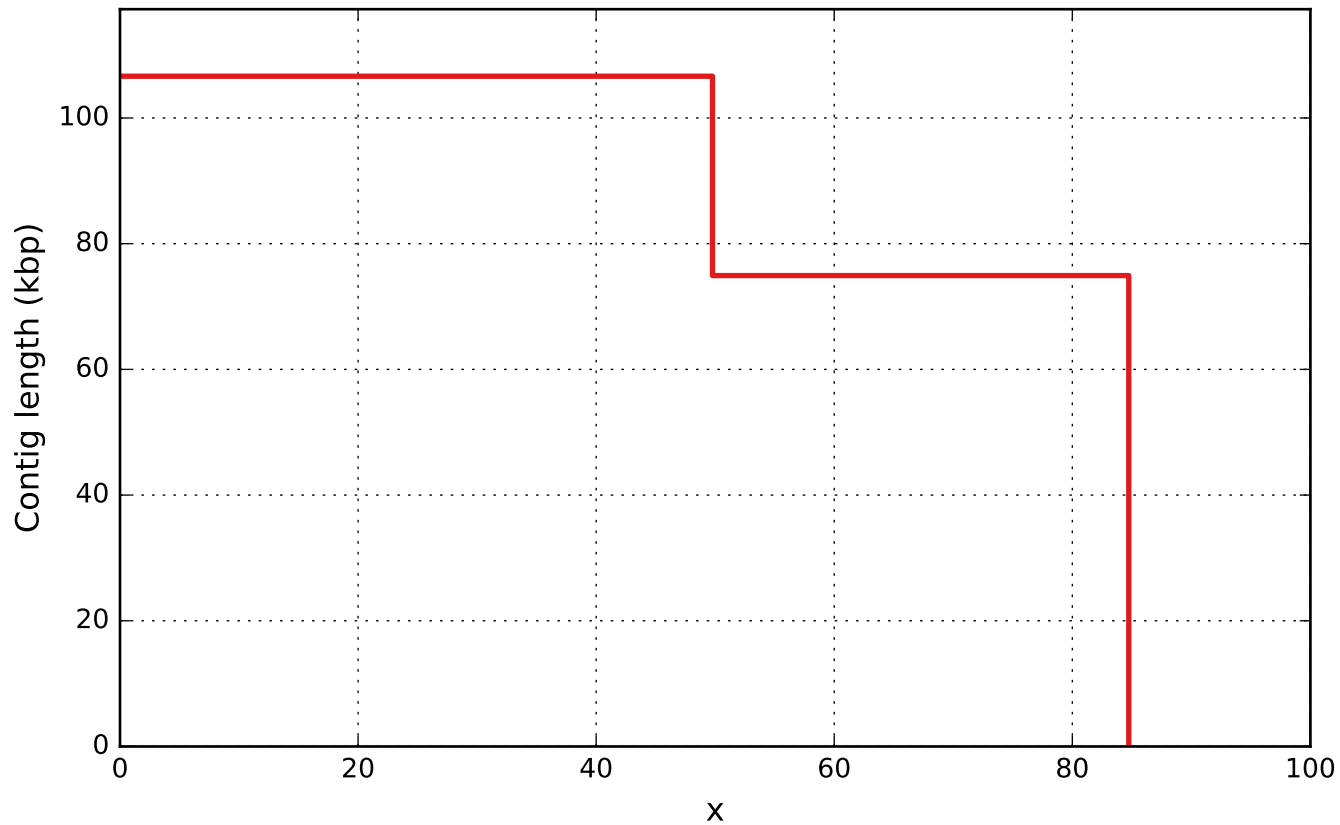


NAx



— mito.contigs.final

NGAx



— mito.contigs.final